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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NOVARTIS AG
- (B) STREET: SCHWARZWALDALLEE 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4058
- (G) TELEPHONE: +41 61 324 11 11
- (H) TELEFAX: + 41 61 322 75 32

(ii) TITLE OF INVENTION: Isolation and Characterization of a Gene

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Oligonucleotide primer DNA (UCPRF)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGACACCG CCAAAGTCCG

20

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Oligonucleotide primer DNA (UCPRR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AGCACACAAA CATGATGACG TTCC

24

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: UCP3L

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCCTGGGATG GAGCCCTAGG GAGCCCCTGT GCTGCCCCTG CCGTGGCAGG ACTCACAGCC	60
CCACCGCTGC ACTGAAGCCC AGGGCTGTGG AGCAGCCTCT CTCCTTGGAC CTCCTCTCGG	120
CCCTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG GACTGAAGCC TTCAGACGTG	180
CCTCCACCA TGGCTGTGAA GTTCCTGGGG GCAGGCACAG CAGCCTGTTT TGCTGACCTC	240
GTTACCTTTC CACTGGACAC AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA GAACCAGGCG	300
GTCCAGACGG CCCGGCTCGT GCAGTACCGT GGCGTGCTGG GCACCATCCT GACCATGGTG	360
CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA GCGCCAGATG	420
AGCTTCGCCT CCATCCGCAT CGGCCTCTAT GACTCCGTCA AGCAGGTGTA CACCCCCAAA	480

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GGCGCGGACA ACTCCAGCCT CACTACCCGG ATTTTGGCCG GCTGCACCAC AGGAGCCATG      540
GCGGTGACCT GTGCCCAGCC CACAGATGTG GTGAAGGTCC GATTTCAGGC CAGCATAACAC      600
CTCGGGCCAT CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC      660
GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAAC TTGCCAACAT CATGAGGAAT      720
GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC TCAAGGAGAA GCTGCTGGAC      780
TACCACCTGC TCACTGACAA CTTCCCTGCG CACTTTGTCT CTGCCTTTGG AGCCGGCTTC      840
TGTGCCACAG TGGTGGCCTC CCCGGTGGAC GTGGTGAAGA CCCGGTATAT GAACTCACCT      900
CCAGGCCAGT ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC      960
ACAGCCTTCT ACAAGGGATT TACACCCTCC TTTTGTGCGT TGGGATCCTG GAACGTGGTG     1020
ATGTTTCGTAA CCTATGAGCA GCTGAAACGG GCCCTGATGA AAGTCCAGAT GTTACGGGAA     1080
TCACCGTTTT GAACAAGACA AGAAGGCCAC TGGTAGCTAA CGTGTCCGAA ACCAGTTAAG     1140
AATGGAAGAA AACGGTGCAT CCACGCACAC ATGGACACAG ACCCACACAT GTTTACAGAA     1200
CTGTTGTTTA CTTGTTGCTG ATTCAAGAAA C                                     1231

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(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: UCP3L
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Gly	Leu	Lys	Pro	Ser	Asp	Val	Pro	Pro	Thr	Met	Ala	Val	Lys
1				5					10					15	
	Phe	Leu	Gly	Ala	Gly	Thr	Ala	Ala	Cys	Phe	Ala	Asp	Leu	Val	Thr

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20	25	30
Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln 35 40 45		
Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr 50 55 60		
Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly 65 70 75 80		
Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile 85 90 95		
Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp 100 105 110		
Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala 115 120 125		
Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe 130 135 140		
Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser 145 150 155 160		
Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg 165 170 175		
Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val 180 185 190		
Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu 195 200 205		
Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala 210 215 220		
Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val 225 230 235 240		
Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro 245 250 255		
Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe 260 265 270		
Tyr Lys Gly Phe Thr Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val 275 280 285		
Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Lys Val 290 295 300		
Gln Met Leu Arg Glu Ser Pro Phe 305 310		

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: UCP3S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TCCTGGGATG GAGCCCTAGG GAGCCCCTGT GCTGCCCCTG CCGTGGCAGG ACTCACAGCC	60
CCACCGCTGC ACTGAAGCCC AGGGCTGTGG AGCAGCCTCT CTCCTTGGAC CTCCTCTCGG	120
CCCTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG GACTGAAGCC TTCAGACGTG	180
CCTCCCACCA TGGCTGTGAA GTTCCTGGGG GCAGGCACAG CAGCCTGTTT TGCTGACCTC	240
GTTACCTTTC CACTGGACAC AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA GAACCAGGCG	300
GTCCAGACGG CCCGGCTCGT GCAGTACCGT GCGGTGCTGG GCACCATCCT GACCATGGTG	360
CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA GCGCCAGATG	420
AGCTTCGCCT CCATCCGCAT CGGCCTCTAT GACTCCGTCA AGCAGGTGTA CACCCCCAAA	480
GGCGCGGACA ACTCCAGCCT CACTACCCGG ATTTTGGCCG GCTGCACCAC AGGAGCCATG	540
GCGGTGACCT GTGCCCAGCC CACAGATGTG GTGAAGGTCC GATTTTCAGGC CAGCATACAC	600
CTCGGGCCAT CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC	660
GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACCT TGCCCAACAT CATGAGGAAT	720
GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC TCAAGGAGAA GCTGCTGGAC	780
TACCACCTGC TCACTGACAA CTTCCCCTGC CACTTTGTCT CTGCCTTTGG AGCCGGCTTC	840
TGTGCCACAG TGGTGGCCTC CCCGGTGGAC GTGGTGAAGA CCCGGTATAT GAACTCACCT	900
CCAGGCCAGT ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC	960

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ACAGCCTTCT ACAAGGGGTG AGCCTCCTCC TGCCTCCAGC ACTCCCTCCC AGAGAACAGG 1020
 GGCTTCTTTC TTTTCGAATG TGGCTACCGT GGGTCAACCT GGGATGTAGC GGTGAAGAGT 1080
 ACAGATGTAA ATGCCACAAA GAAGAAGTTT AAAAAACCAT GCAAAAAAAAA AA 1132

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: UCP3S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Val	Gly	Leu	Lys	Pro	Ser	Asp	Val	Pro	Pro	Thr	Met	Ala	Val	Lys	1	5	10	15
Phe	Leu	Gly	Ala	Gly	Thr	Ala	Ala	Cys	Phe	Ala	Asp	Leu	Val	Thr	Phe	20	25	30	
Pro	Leu	Asp	Thr	Ala	Lys	Val	Arg	Leu	Gln	Ile	Gln	Gly	Glu	Asn	Gln	35	40	45	
Ala	Val	Gln	Thr	Ala	Arg	Leu	Val	Gln	Tyr	Arg	Gly	Val	Leu	Gly	Thr	50	55	60	
Ile	Leu	Thr	Met	Val	Arg	Thr	Glu	Gly	Pro	Cys	Ser	Pro	Tyr	Asn	Gly	65	70	75	80
Leu	Val	Ala	Gly	Leu	Gln	Arg	Gln	Met	Ser	Phe	Ala	Ser	Ile	Arg	Ile	85	90	95	
Gly	Leu	Tyr	Asp	Ser	Val	Lys	Gln	Val	Tyr	Thr	Pro	Lys	Gly	Ala	Asp	100	105	110	
Asn	Ser	Ser	Leu	Thr	Thr	Arg	Ile	Leu	Ala	Gly	Cys	Thr	Thr	Gly	Ala	115	120	125	
Met	Ala	Val	Thr	Cys	Ala	Gln	Pro	Thr	Asp	Val	Val	Lys	Val	Arg	Phe				

[illegible]